

SEQUENCE LISTING

<110> Cochran, Mark D
Cook, Stephanie M
Wild, Martha A

<120> Novel Avian Herpes Virus and Uses Thereof

<130> SY01105K1QKQK

<140> xxxxxxxxxxxxx

<141> 2001-06-14

<150> 09/426,352

<151> 1999-10-25

<150> 08/804,372

<151> 1997-02-21

<150> PCT/US95/10245

<151> 1995-08-09

<150> 08/663,566

<151> 1996-06-13

<150> 08/288,065

<151> 1994-08-09

<150> PCT/US93/05681

<151> 1993-06-14

<150> 08/023,610

<151> 1993-02-26

<150> 07/898,087

<151> 1992-06-12

<160> 5

<170> PatentIn Ver. 2.1

<210> 1

<211> 3570

<212> DNA

<213> Newcastle disease virus

<220>

<221> CDS

<222> (1194)..(2888)

<223> NDV Fusion Protein

<400> 1

```
gtacgttaat taaccgcgga agcttgcatg cctgcagtga ataataaaat gtgtgtttgt 60
ccgaaatacg cgttttgaga tttctgtcgc cgactaaatt catgtcgcgc gatagtgggtg 120
tttatcgccg atagagatgg cgatattgga aaaatcgata ttgaaaata tggcatattg 180
aaaatgtcgc cgatgtgagt ttctgtgtaa ctgatatctg gcgatagcgc ttatatcggt 240
tacgggggat ggcgatagac gactttggcg acttgggcga ttctgtgtgt cgcaaataac 300
gcagtttcga tataggtagc agacgatatg aggctatata gccgatagag gcgacatcaa 360
gctggcacat ggccaatgca tatcgatcta tacattgaat caatattggc aattagccat 420
attagtcatt gggttatatag cataaatcaa tattggctat tggccattgc atacgttgta 480
tctatatcat aatatgtaca tttatattgg ctcatgtcca atatgaccgc catgttgaca 540
```

09001457 061401

ttgattatttg actagtttatt aatagtaatc aattacgggg tcattagttc atagcccata																600
tatggagttc cgcgttacat aacttacggt aaatggcccg cctggctgac cgcccaacga																660
ccccgcccc ttgacgtcaa taatgacgta tgttcccata gtaacgccaa tagggacttt																720
ccattgacgt caatgggtgg agtattttacg gtaaactgcc cacttggcag tacatcaagt																780
gtatcatatg ccaagtcgcg cccctattga cgtcaatgac ggtaaattggc ccgcctggca																840
ttatgcccg tacatgacct tacgggactt tctacttgg cagtacatct acgtattagt																900
catcgctatt accatggtga tgcggttttg gcagtacacc aatgggcgtg gatagcggtt																960
tgactcacgg ggatttccaa gtctccaccc cattgacgtc aatgggagtt tgttttggca																1020
ccaaaatcaa cgggactttc caaaatgtcg taataacccc gcccgttga cgcaaatggg																1080
cggtaggcgt gtacggtggg aggtctatat aagcagagct cgtttagtga accgtcagat																1140
cgcttgaga cgccatccac gctgttttga cctccataga agacaccggg acc atg																1196
																Met 1
gat cga tcc cgg ttg gcg ccc tcc agg tgc agg atg ggc tcc aga cct																1244
Asp Arg Ser Arg 5 Leu Ala Pro Ser Arg 10 Cys Arg Met Gly Ser 15 Arg Pro																
tct acc aag aac cca gca cct atg atg ctg act atc cgg gtc gcg ctg																1292
Ser Thr Lys 20 Asn Pro Ala Pro Met 25 Met Leu Thr Ile Arg 30 Val Ala Leu																
gta ctg agt tgc atc tgt ccg gca aac tcc att gat ggc agg cct ctt																1340
Val Leu Ser 35 Cys Ile Cys Pro Ala Asn Ser Ile Asp 45 Gly Arg Pro Leu																
gca gct gca gga ctn tgg tta cag gag aca aag caa tca aca tat aca																1388
Ala Ala Ala Gly Xaa Trp 55 Leu Gln Glu Thr Lys 60 Gln Ser Thr Tyr Thr 65																
cct cat ccc aga cag gtc aat cat att aag ctc ctc ccg aat ctg cca																1436
Pro His Pro Arg 70 Gln Val Asn His Ile Lys 75 Leu Leu Pro Asn Leu Pro 80																
aag gat aag gag gca tgt gcg aaa gcc ccc ttg gat gca tac aac agg																1484
Lys Asp Lys Glu Ala Cys Ala Lys Ala Pro Leu Asp Ala Tyr 95 Asn Arg																
aca ttg acc act ttg ctc acc ccc ctt ggt gac tct atc cgt agg ata																1532
Thr Leu Thr 100 Thr Leu Leu Thr Pro 105 Leu Gly Asp Ser Ile Arg Arg Ile																
caa gag tct gtg act aca tct gga ggg ggg aga cag ggg cgc ctt ata																1580
Gln Glu Ser Val Thr Thr Ser Gly Gly Gly Arg Gln Gly Arg Leu Ile																
ggc gcc att att ggc ggt gtg gct ctt ggg gtt gca act gcc gca caa																1628
Gly Ala Ile Ile Gly Gly Val Ala Leu Gly Val 140 Ala Thr Ala Ala Gln 145																
ata aca gcg gcc gca gct ctg ata caa gcc aaa caa aat gct gcc aac																1676
Ile Thr Ala Ala 150 Ala Leu Ile Gln 155 Ala Lys Gln Asn Ala Ala Asn 160																
atc ctc cga ctt aaa gag agc att gcc gca acc aat gag gct gtg cat																1724
Ile Leu Arg 165 Lys Glu Ser Ile 170 Ala Ala Thr Asn Glu Ala Val His 175																

gag gtc act gac gga tta tcg caa cta gca gtg gca gtt ggg aag atg	1772
Glu Val Thr Asp Gly Leu Ser Gln Leu Ala Val Ala Val Gly Lys Met	
180 185 190	
cag cag ttc gtt aat gac caa ttt aat aaa aca gct cag gaa tta gac	1820
Gln Gln Phe Val Asn Asp Gln Phe Asn Lys Thr Ala Gln Glu Leu Asp	
195 200 205	
tgc atc aaa att gca cag caa gtt ggt gta gag ctc aac ctg tac cta	1868
Cys Ile Lys Ile Ala Gln Gln Val Gly Val Glu Leu Asn Leu Tyr Leu	
210 215 220 225	
acc gaa tcg act aca gta ttc gga cca caa atc act tca cct gcc tta	1916
Thr Glu Ser Thr Thr Val Phe Gly Pro Gln Ile Thr Ser Pro Ala Leu	
230 235 240	
aac aag ctg act att cag gca ctt tac aat cta gct ggt ggg aat atg	1964
Asn Lys Leu Thr Thr Ile Gln Ala Leu Tyr Asn Leu Ala Gly Asn Met	
245 250 255	
gat tac tta ttg act aag tta ggt ata ggg aac aat caa ctc agc tca	2012
Asp Tyr Leu Leu Thr Lys Leu Gly Ile Gly Asn Asn Gln Leu Ser Ser	
260 265 270	
tta atc ggt agc ggc tta atc acc ggt aac cct att cta tac gac tca	2060
Leu Ile Gly Ser Gly Leu Ile Thr Gly Asn Pro Ile Leu Tyr Asp Ser	
275 280 285	
cag act caa ctc ttg ggt ata cag gta act cta cct tca gtc ggg aac	2108
Gln Thr Gln Leu Leu Gly Ile Gln Val Thr Leu Pro Ser Val Gly Asn	
290 295 300 305	
cta aat aat atg cgt gcc acc tac ttg gaa acc tta tcc gta agc aca	2156
Leu Asn Asn Met Arg Ala Thr Tyr Leu Glu Thr Leu Ser Val Ser Thr	
310 315 320	
acc agg gga ttt gcc tcg gca ctt gtc cca aaa gtg gtg aca cgg gtc	2204
Thr Arg Gly Phe Ala Ser Ala Leu Val Pro Lys Val Val Thr Arg Val	
325 330 335	
ggt tct gtg ata gaa gaa ctt gac acc tca tac tgt ata gaa act gac	2252
Gly Ser Val Ile Glu Glu Leu Asp Thr Ser Tyr Cys Ile Glu Thr Asp	
340 345 350	
tta gat tta tat tgt aca aga ata gta acg ttc cct atg tcc cct ggt	2300
Leu Asp Leu Tyr Cys Thr Arg Ile Val Thr Phe Pro Met Ser Pro Gly	
355 360 365	
att tac tcc tgc ttg agc ggc aat aca tcg gcc tgt atg tac tca aag	2348
Ile Tyr Ser Cys Leu Ser Gly Asn Thr Ser Ala Cys Met Tyr Ser Lys	
370 375 380 385	
acc gaa ggc gca ctt act aca cca tat atg act atc aaa ggc tca gtc	2396
Thr Glu Gly Ala Leu Thr Thr Pro Tyr Met Thr Ile Lys Gly Ser Val	
390 395 400	
atc gct aac tgc aag atg aca aca tgt aga tgt gta aac ccc ccg ggt	2444
Ile Ala Asn Cys Lys Met Thr Thr Cys Arg Cys Val Asn Pro Pro Gly	
405 410 415	
atc ata tcg caa aac tat gga gaa gcc gtg tct cta ata gat aaa caa	2492
Ile Ile Ser Gln Asn Tyr Gly Glu Ala Val Ser Leu Ile Asp Lys Gln	
420 425 430	
tca tgc aat gtt tta tcc tta ggc ggg ata act tta agg ctc agt ggg	2540
Ser Cys Asn Val Leu Ser Leu Gly Gly Ile Thr Leu Arg Leu Ser Gly	
435 440 445	
gaa ttc gat gta act tat cag aag aat atc tca ata caa gat tct caa	2588

09081457 061401

Glu Phe Asp Val Thr Tyr Gln Lys Asn Ile Ser Ile Gln Asp Ser Gln
 450 455 460 465
 gta ata ata aca ggc aat ctt gat atc tca act gag ctt ggg aat gtc 2636
 Val Ile Ile Thr Gly Asn Leu Asp Ile Ser Thr Glu Leu Gly Asn Val 470 475 480
 aac aac tcg atc agt aat gcc ttg aat aag tta gag gaa agc aac aga 2684
 Asn Asn Ser Ile Ser Asn Ala Leu Asn Lys Leu Glu Glu Ser Asn Arg 485 490 495
 aaa cta gac aaa gtc aat gtc aaa ctg acc agc aca tct gct ctc att 2732
 Lys Leu Asp Lys Val Asn Val Lys Leu Thr Ser Thr Phe Ser Ala Leu Ile 500 505 510
 acc tat atc gtt ttg act atc ata tct ctt gtt ttt ggt ata ctt agc 2780
 Thr Tyr Ile Val Leu Thr Ile Ile Ser Leu Val Phe Gly Ile Leu Ser 515 520 525
 ctg att cta gca tgc tac cta atg tac aag caa aag gcg caa caa aag 2828
 Leu Ile Leu Ala Cys Tyr Leu Met Tyr Lys Gln Lys Ala Gln Gln Lys 530 535 540 545
 acc tta tta tgg ctt ggg aat aat acc cta gat cag atg aga gcc act 2876
 Thr Leu Leu Trp Leu Gly Asn Asn Thr Leu Asp Gln Met Arg Ala Thr 550 555 560
 aca aaa atg tga acacagatga ggaacgaagg tttccctaata agtaatttgt 2928
 Thr Lys Met 565
 gtgaaagtgc tggtagtctg tcagttcgga gagttaagaa aaaaaaaaaa ccccccccc 2988
 ccccccccc cccccctggg tacgatcctc tagagtcggg agatggggga ggctaactga 3048
 aacacggaag gagacaatac cggaaggaac ccgcgctatg acggcaataa aaagacagaa 3108
 taaaacgcac ggggtgttggg tcgtttgttc ataaacgcgg ggttcgggtcc cagggctggc 3168
 actctgtcga taccaccacg agaccaccatt gggaccaata cgcgcgctt tcttcctttt 3228
 cccaccccca acccccaagt tcgggtgaag gccagggct cgcagccaac gtcggggcgg 3288
 caagccctgc catagccacg ggccccgtgg gttagggacg gggccccca tggggaatgg 3348
 tttatgggtc gtgggggtta ttattttggg cgttgctggg ggtcaggtcc acgactggac 3408
 tgagcagaca gaccatggt ttttgatgg cctgggcatg gaccgcatgt actggcgcga 3468
 cacgaacacc gggcgtctgt ggctgcaaaa ccccccgac ccccaaaaac caccgcgcgg 3528
 atttctggcg ccgccggacg tcgacttaata taacaagctt ag 3570

 <210> 2
 <211> 564
 <212> PRT
 <213> Newcastle disease virus

 <400> 2
 Met Asp Arg Ser Arg Leu Ala Pro Ser Arg Cys Arg Met Gly Ser Arg
 1 5 10 15
 Pro Ser Thr Lys Asn Pro Ala Pro Met Met Leu Thr Ile Arg Val Ala
 20 25 30
 Leu Val Leu Ser Cys Ile Cys Pro Ala Asn Ser Ile Asp Gly Arg Pro
 35 40 45

0981457 061401

Leu	Ala	Ala	Ala	Gly	Xaa	Trp	Leu	Gln	Glu	Thr	Lys	Gln	Ser	Thr	Tyr
50						55					60				
Thr	Pro	His	Pro	Arg	Gln	Val	Asn	His	Ile	Lys	Leu	Leu	Pro	Asn	Leu
65					70					75					80
Pro	Lys	Asp	Lys	Glu	Ala	Cys	Ala	Lys	Ala	Pro	Leu	Asp	Ala	Tyr	Asn
				85					90					95	
Arg	Thr	Leu	Thr	Thr	Leu	Leu	Thr	Pro	Leu	Gly	Asp	Ser	Ile	Arg	Arg
			100					105					110		
Ile	Gln	Glu	Ser	Val	Thr	Thr	Ser	Gly	Gly	Gly	Arg	Gln	Gly	Arg	Leu
		115					120					125			
Ile	Gly	Ala	Ile	Ile	Gly	Gly	Val	Ala	Leu	Gly	Val	Ala	Thr	Ala	Ala
	130					135					140				
Gln	Ile	Thr	Ala	Ala	Ala	Ala	Leu	Ile	Gln	Ala	Lys	Gln	Asn	Ala	Ala
145					150					155					160
Asn	Ile	Leu	Arg	Leu	Lys	Glu	Ser	Ile	Ala	Ala	Thr	Asn	Glu	Ala	Val
				165					170					175	
His	Glu	Val	Thr	Asp	Gly	Leu	Ser	Gln	Leu	Ala	Val	Ala	Val	Gly	Lys
			180					185					190		
Met	Gln	Gln	Phe	Val	Asn	Asp	Gln	Phe	Asn	Lys	Thr	Ala	Gln	Glu	Leu
		195					200					205			
Asp	Cys	Ile	Lys	Ile	Ala	Gln	Gln	Val	Gly	Val	Glu	Leu	Asn	Leu	Tyr
	210					215					220				
Leu	Thr	Glu	Ser	Thr	Thr	Val	Phe	Gly	Pro	Gln	Ile	Thr	Ser	Pro	Ala
225					230					235					240
Leu	Asn	Lys	Leu	Thr	Ile	Gln	Ala	Leu	Tyr	Asn	Leu	Ala	Gly	Gly	Asn
				245					250					255	
Met	Asp	Tyr	Leu	Leu	Thr	Lys	Leu	Gly	Ile	Gly	Asn	Asn	Gln	Leu	Ser
			260					265					270		
Ser	Leu	Ile	Gly	Ser	Gly	Leu	Ile	Thr	Gly	Asn	Pro	Ile	Leu	Tyr	Asp
		275					280					285			
Ser	Gln	Thr	Gln	Leu	Leu	Gly	Ile	Gln	Val	Thr	Leu	Pro	Ser	Val	Gly
	290					295					300				
Asn	Leu	Asn	Asn	Met	Arg	Ala	Thr	Tyr	Leu	Glu	Thr	Leu	Ser	Val	Ser
305					310					315					320
Thr	Thr	Arg	Gly	Phe	Ala	Ser	Ala	Leu	Val	Pro	Lys	Val	Val	Thr	Arg
				325					330					335	
Val	Gly	Ser	Val	Ile	Glu	Glu	Leu	Asp	Thr	Ser	Tyr	Cys	Ile	Glu	Thr
			340					345					350		
Asp	Leu	Asp	Leu	Tyr	Cys	Thr	Arg	Ile	Val	Thr	Phe	Pro	Met	Ser	Pro
		355					360					365			
Gly	Ile	Tyr	Ser	Cys	Leu	Ser	Gly	Asn	Thr	Ser	Ala	Cys	Met	Tyr	Ser
	370					375					380				
Lys	Thr	Glu	Gly	Ala	Leu	Thr	Thr	Pro	Tyr	Met	Thr	Ile	Lys	Gly	Ser
385					390					395					400
Val	Ile	Ala	Asn	Cys	Lys	Met	Thr	Thr	Cys	Arg	Cys	Val	Asn	Pro	Pro
				405					410					415	

09881457 061401

```
<210> 3
<211> 3605
<212> DNA
<213> Infectious Laryngotracheitis Virus
```

```
<220>
<221> CDS
<222> (1997)..(3085)
<223> ILTV glycoprotein I
```

Met His Arg Pro

cat	ctc	aga	cgg	cac	tcg	cgt	tac	tac	gcg	aaa	gga	gag	gtg	ctt	aac	644
His	Leu	Arg	Arg	His	Ser	Arg	Tyr	Tyr	Ala	Lys	Gly	Glu	Val	Leu	Asn	
5					10					15					20	
aaa	cac	atg	gat	tgc	ggg	gga	aaa	cgg	tgc	tgc	tca	ggc	gca	gct	gta	692
Lys	His	Met	Asp	Cys	Gly	Gly	Lys	Arg	Cys	Cys	Ser	Gly	Ala	Ala	Val	
				25					30					35		
ttc	act	ctt	ttc	tgg	act	tgt	gtc	agg	att	atg	cgg	gag	cat	atc	tgc	740
Phe	Thr	Leu	Phe	Trp	Thr	Cys	Val	Arg	Ile	Met	Arg	Glu	His	Ile	Cys	
			40					45					50			
ttt	gta	cgc	aac	gct	atg	gac	cgc	cat	tta	ttt	ttg	agg	aat	gct	ttt	788
Phe	Val	Arg	Asn	Ala	Met	Asp	Arg	His	Leu	Phe	Leu	Arg	Asn	Ala	Phe	
		55					60					65				
tgg	act	atc	gta	ctg	ctt	tct	tcc	ttc	gct	agc	cag	agc	acc	gcc	gcc	836
Trp	Thr	Ile	Val	Leu	Leu	Ser	Ser	Phe	Ala	Ser	Gln	Ser	Thr	Ala	Ala	
	70					75					80					
gtc	acg	tac	gac	tac	att	tta	ggc	cgt	cgc	gcg	ctc	gac	gcg	cta	acc	884
Val	Thr	Tyr	Asp	Tyr	Ile	Leu	Gly	Arg	Arg	Ala	Leu	Asp	Ala	Leu	Thr	
85					90				95						100	
ata	ccg	gcg	gtt	ggc	ccg	tat	aac	aga	tac	ctc	act	agg	gta	tca	aga	932
Ile	Pro	Ala	Val	Gly	Pro	Tyr	Asn	Arg	Tyr	Leu	Thr	Arg	Val	Ser	Arg	
				105					110					115		
ggc	tgc	gac	gtt	gtc	gag	ctc	aac	ccg	att	tct	aac	gtg	gac	gac	atg	980
Gly	Cys	Asp	Val	Val	Glu	Leu	Asn	Pro	Ile	Ser	Asn	Val	Asp	Asp	Met	
			120					125					130			
ata	tcg	gcg	gcc	aaa	gaa	aaa	gag	aag	ggg	ggc	cct	ttc	gag	gcc	tcc	1028
Ile	Ser	Ala	Ala	Lys	Glu	Lys	Glu	Lys	Gly	Gly	Pro	Phe	Glu	Ala	Ser	
		135					140					145				
gtc	gtc	tgg	ttc	tac	gtg	att	aag	ggc	gac	gac	ggc	gag	gac	aag	tac	1076
Val	Val	Trp	Phe	Tyr	Val	Ile	Lys	Gly	Asp	Asp	Gly	Glu	Asp	Lys	Tyr	
	150					155					160					
tgt	cca	atc	tat	aga	aaa	gag	tac	agg	gaa	tgt	ggc	gac	gta	caa	ctg	1124
Cys	Pro	Ile	Tyr	Arg	Lys	Glu	Tyr	Arg	Glu	Cys	Gly	Asp	Val	Gln	Leu	
165					170					175					180	
cta	tct	gaa	tgc	gcc	gtt	caa	tct	gca	cag	atg	tgg	gca	gtg	gac	tat	1172
Leu	Ser	Glu	Cys	Ala	Val	Gln	Ser	Ala	Gln	Met	Trp	Ala	Val	Asp	Tyr	
				185					190					195		
gtt	cct	agc	acc	ctt	gta	tcg	cga	aat	ggc	gcg	gga	ctg	act	ata	ttc	1220
Val	Pro	Ser	Thr	Leu	Val	Ser	Arg	Asn	Gly	Ala	Gly	Leu	Thr	Ile	Phe	
			200					205					210			
tcc	ccc	act	gct	gcg	ctc	tct	ggc	caa	tac	ttg	ctg	acc	ctg	aaa	atc	1268
Ser	Pro	Thr	Ala	Ala	Leu	Ser	Gly	Gln	Tyr	Leu	Leu	Thr	Leu	Lys	Ile	
		215					220					225				
ggg	aga	ttt	gcg	caa	aca	gct	ctc	gta	act	cta	gaa	gtt	aac	gat	cgc	1316
Gly	Arg	Phe	Ala	Gln	Thr	Ala	Leu	Val	Thr	Leu	Glu	Val	Asn	Asp	Arg	
	230					235					240					
tgt	tta	aag	atc	ggg	tcg	cag	ctt	aac	ttt	tta	ccg	tcg	aaa	tgc	tgg	1364
Cys	Leu	Lys	Ile	Gly	Ser	Gln	Leu	Asn	Phe	Leu	Pro	Ser	Lys	Cys	Trp	
245					250					255					260	
aca	aca	gaa	cag	tat	cag	act	gga	ttt	caa	ggc	gaa	cac	ctt	tat	ccg	1412
Thr	Thr	Glu	Gln	Tyr	Gln	Thr	Gly	Phe	Gln	Gly	Glu	His	Leu	Tyr	Pro	
				265					270					275		
atc	gca	gac	acc	aat	aca	cga	cac	gcg	gac	gac	gta	tat	cgg	gga	tac	1460

05881457 061401

Ile	Ala	Asp	Thr	Asn	Thr	Arg	His	Ala	Asp	Asp	Val	Tyr	Arg	Gly	Tyr		
			280					285					290				
gaa	gat	att	ctg	cag	cgc	tgg	aat	aat	ttg	ctg	agg	aaa	aag	aat	cct	1508	
Glu	Asp	Ile	Leu	Gln	Arg	Trp	Asn	Asn	Leu	Leu	Arg	Lys	Lys	Asn	Pro		
		295					300					305					
agc	gcg	cca	gac	cct	cgt	cca	gat	agc	gtc	ccg	caa	gaa	att	ccc	gct	1556	
Ser	Ala	Pro	Asp	Pro	Arg	Pro	Asp	Ser	Val	Pro	Gln	Glu	Ile	Pro	Ala		
	310					315					320						
gta	acc	aag	aaa	gcg	gaa	ggg	cgc	acc	ccg	gac	gca	gaa	agc	agc	gaa	1604	
Val	Thr	Lys	Lys	Ala	Glu	Gly	Arg	Thr	Pro	Asp	Ala	Glu	Ser	Ser	Glu		
	325				330					335					340		
aag	aag	gcc	cct	cca	gaa	gac	tcg	gag	gac	gac	atg	cag	gca	gag	gct	1652	
Lys	Lys	Ala	Pro	Pro	Glu	Asp	Ser	Glu	Asp	Asp	Met	Gln	Ala	Glu	Ala		
				345					350					355			
tct	gga	gaa	aat	cct	gcc	gcc	ctc	ccc	gaa	gac	gac	gaa	gtc	ccc	gag	1700	
Ser	Gly	Glu	Asn	Pro	Ala	Ala	Leu	Pro	Glu	Asp	Asp	Glu	Val	Pro	Glu		
			360					365					370				
gac	acc	gag	cac	gat	gat	cca	aac	tcg	gat	cct	gac	tat	tac	aat	gac	1748	
Asp	Thr	Glu	His	Asp	Asp	Pro	Asn	Ser	Asp	Pro	Asp	Tyr	Tyr	Asn	Asp		
		375					380					385					
atg	ccc	gcc	gtg	atc	ccg	gtg	gag	gag	act	act	aaa	agt	tct	aat	gcc	1796	
Met	Pro	Ala	Val	Ile	Pro	Val	Glu	Glu	Thr	Thr	Lys	Ser	Ser	Asn	Ala		
	390					395					400						
gtc	tcc	atg	ccc	ata	ttc	gcg	gcg	ttc	gta	gcc	tgc	gcg	gtc	gcg	ctc	1844	
Val	Ser	Met	Pro	Ile	Phe	Ala	Ala	Phe	Val	Ala	Cys	Ala	Val	Ala	Leu		
	405				410					415					420		
gtg	ggg	cta	ctg	gtt	tgg	agc	atc	gta	aaa	tgc	gcg	cgt	agc	taa		1889	
Val	Gly	Leu	Leu	Val	Trp	Ser	Ile	Val	Lys	Cys	Ala	Arg	Ser				
				425					430					435			
tcgagcctag	aataggtggt	ttcttcctac	atgccacgcc	tcacgctcat	aatataaatc											1949	
acatggaata	gcataccaat	gcctattcat	tgggacgttc	gaaaagc	atg	gca	tcg									2005	
				Met	Ala	Ser											
cta	ctt	gga	act	ctg	gct	ctc	ctt	gcc	gcg	acg	ctc	gca	ccc	ttc	ggc	2053	
Leu	Leu	Gly	Thr	Leu	Ala	Leu	Leu	Ala	Ala	Thr	Leu	Ala	Pro	Phe	Gly		
	440					445					450						
gcg	atg	gga	atc	gtg	atc	act	gga	aat	cac	gtc	tcc	gcc	agg	att	gac	2101	
Ala	Met	Gly	Ile	Val	Ile	Thr	Gly	Asn	His	Val	Ser	Ala	Arg	Ile	Asp		
	455				460					465					470		
gac	gat	cac	atc	gtg	atc	gtc	gcg	cct	cgc	ccc	gaa	gct	aca	att	caa	2149	
Asp	Asp	His	Ile	Val	Ile	Val	Ala	Pro	Arg	Pro	Glu	Ala	Thr	Ile	Gln		
				475					480					485			
ctg	cag	cta	ttt	ttc	atg	cct	ggc	cag	aga	ccc	cac	aaa	ccc	tac	tca	2197	
Leu	Gln	Leu	Phe	Phe	Met	Pro	Gly	Gln	Arg	Pro	His	Lys	Pro	Tyr	Ser		
			490					495					500				
gga	acc	gtc	cgc	gtc	gcg	ttt	cgg	tct	gat	ata	aca	aac	cag	tgc	tac	2245	
Gly	Thr	Val	Arg	Val	Ala	Phe	Arg	Ser	Asp	Ile	Thr	Asn	Gln	Cys	Tyr		
		505					510					515					
cag	gaa	ctt	agc	gag	gag	cgc	ttt	gaa	aat	tgc	act	cat	cga	tcg	tct	2293	
Gln	Glu	Leu	Ser	Glu	Glu	Arg	Phe	Glu	Asn	Cys	Thr	His	Arg	Ser	Ser		
	520					525					530						
tct	gtt	ttt	gtc	ggc	tgt	aaa	gtg	acc	gag	tac	acg	ttc	tcc	gcc	tcg	2341	

09881457-061401

Ser 535	Val	Phe	Val	Gly	Cys 540	Lys	Val	Thr	Glu	Tyr 545	Thr	Phe	Ser	Ala	Ser 550	
aac Asn	aga Arg	cta Leu	acc Thr	gga Gly 555	cct Pro	cca Pro	cac His	ccg Pro	ttt Phe 560	aag Lys	ctc Leu	act Thr	ata Ile	cga Arg 565	aat Asn	2389
cct Pro	cgt Arg	ccg Pro	aac Asn 570	gac Asp	agc Ser	ggg Gly	atg Met	ttc Phe 575	tac Tyr	gta Val	att Ile	gtt Val	cgg Arg 580	cta Leu	gac Asp	2437
gac Asp	acc Thr	aaa Lys 585	gaa Glu	ccc Pro	att Ile	gac Asp	gtc Val 590	ttc Phe	gcg Ala	atc Ile	caa Gln	cta Ser 595	tcg Val	gtg Val	tat Tyr	2485
caa Gln	ttc Phe 600	gcg Ala	aac Asn	acc Thr	gcc Ala	gcg Ala 605	act Thr	cgc Arg	gga Gly	ctc Leu	tat Tyr 610	tcc Ser	aag Lys	gct Ala	tcg Ser	2533
tgt Cys 615	cgc Arg	acc Thr	ttc Phe	gga Gly 620	tta Leu 620	cct Pro	acc Thr	gtc Val	caa Gln	ctt Leu 625	gag Glu	gcc Ala	tat Tyr	ctc Leu	agg Arg 630	2581
acc Thr	gag Glu	gaa Glu	agt Ser	tgg Trp 635	cgc Arg	aac Asn	tgg Trp	caa Gln	gcg Ala 640	tac Tyr	gtt Val	gcc Ala	acg Thr	gag Glu 645	gcc Ala	2629
acg Thr	acg Thr	acc Thr	agc Ser 650	gcc Ala	gag Glu	gcg Ala	aca Thr	acc Thr	ccg Pro	acg Thr	ccc Pro	gtc Val	act Thr 660	gca Ala	acc Thr	2677
agc Ser	gcc Ala	tcc Ser 665	gaa Glu	ctt Leu	gaa Glu	gcg Ala	gaa Glu 670	cac His	ttt Phe	acc Thr	ttt Phe	ccc Pro 675	tgg Trp	cta Leu	gaa Glu	2725
aat Asn	ggc Gly 680	gtg Val	gat Asp	cat His	tac Tyr	gaa Glu 685	ccg Pro	aca Thr	ccc Pro	gca Ala	aac Asn 690	gaa Glu	aat Asn	tca Ser	aac Asn	2773
gtt Val 695	act Thr	gtc Val	cgt Arg	ctc Leu	ggg Gly 700	aca Thr	atg Met	agc Ser	cct Pro	acg Thr 705	cta Leu	att Ile	ggg Gly	gta Val 710	acc Thr	2821
gtg Val	gct Ala	gcc Ala	gtc Val	gtg Val 715	agc Ser	gca Ala	acg Thr	atc Ile	ggc Gly 720	ctc Leu	gtc Val	att Ile	gta Val 725	att Ile	tcc Ser	2869
atc Ile	gtc Val	acc Thr	aga Arg 730	aac Asn	atg Met	tgc Cys	acc Thr	ccg Pro 735	cac His	cga Arg	aaa Lys	tta Leu	gac Asp 740	acg Thr	gtc Val	2917
tcg Ser	caa Gln	gac Asp 745	gac Asp	gaa Glu	gaa Glu	cgt Arg	tcc Ser 750	caa Gln	act Thr	aga Arg	agg Arg	gaa Glu 755	tcg Ser	cga Arg	aaa Lys	2965
ttt Phe 760	gga Gly	ccc Pro	atg Met	gtt Val	gcg Ala	tgc Cys 765	gaa Glu	ata Ile	aac Asn	aag Lys	ggg Gly 770	gct Ala	gac Asp	cag Gln	gat Asp	3013
agt Ser 775	gaa Glu	ctt Leu	gtg Val	gaa Glu	ctg Leu 780	gtt Val	gcg Ala	att Ile	gtt Val	aac Asn 785	ccg Pro	tct Ser	gcg Ala	cta Leu	agc Ser 790	3061
tcg Ser	ccc Pro	gac Asp	tca Ser	ata Ile	aaa Lys	atg Met	tga	ttaagtctga	atgtggctct	ccaatcattt						3115
cgattctcta	atctcccaat	cctctcaaaa	ggggcagtat	cggacacgga	ctgggagggg											3175

T04T90"254T8860

cgtacacgat agttatatgg tacagcagag gcctctgaac acttaggagg agaattcagc 3235
 cggggagagc ccctgttgag taggcttggg agcatattgc aggatgaaca tgtagtgat 3295
 agttctcgcc tcttgtcttg cgcgcctaac ttttgcgacg cgacacgtcc tctttttgga 3355
 aggcaactcag gctgtcctcg gggaagatga tcccagaaac gttccggaag ggactgtaat 3415
 caaatggaca aaagtccctgc ggaacgcgtg caagatgaag gcggccgatg tctgctcttc 3475
 gcctaactat tgctttcatg atttaattta cgacggagga aagaaagact gcccgccgc 3535
 gggacccttg tctgcaaacc tggtaat ttt actaaagcgc ggcgaaagct tcccgggtta 3595
 attaacgtac 3605

<210> 4
 <211> 434
 <212> PRT
 <213> Infectious Laryngotracheitis Virus

<400> 4
 Met His Arg Pro His Leu Arg Arg His Ser Arg Tyr Tyr Ala Lys Gly
 1 5 10 15
 Glu Val Leu Asn Lys His Met Asp Cys Gly Gly Lys Arg Cys Cys Ser
 20 25 30
 Gly Ala Ala Val Phe Thr Leu Phe Trp Thr Cys Val Arg Ile Met Arg
 35 40 45
 Glu His Ile Cys Phe Val Arg Asn Ala Met Asp Arg His Leu Phe Leu
 50 55 60
 Arg Asn Ala Phe Trp Thr Ile Val Leu Leu Ser Ser Phe Ala Ser Gln
 65 70 75 80
 Ser Thr Ala Ala Val Thr Tyr Asp Tyr Ile Leu Gly Arg Arg Ala Leu
 85 90 95
 Asp Ala Leu Thr Ile Pro Ala Val Gly Pro Tyr Asn Arg Tyr Leu Thr
 100 105 110
 Arg Val Ser Arg Gly Cys Asp Val Val Glu Leu Asn Pro Ile Ser Asn
 115 120 125
 Val Asp Asp Met Ile Ser Ala Ala Lys Glu Lys Glu Lys Gly Gly Pro
 130 135 140
 Phe Glu Ala Ser Val Val Trp Phe Tyr Val Ile Lys Gly Asp Asp Gly
 145 150 155 160
 Glu Asp Lys Tyr Cys Pro Ile Tyr Arg Lys Glu Tyr Arg Glu Cys Gly
 165 170 175
 Asp Val Gln Leu Leu Ser Glu Cys Ala Val Gln Ser Ala Gln Met Trp
 180 185 190
 Ala Val Asp Tyr Val Pro Ser Thr Leu Val Ser Arg Asn Gly Ala Gly
 195 200 205
 Leu Thr Ile Phe Ser Pro Thr Ala Ala Leu Ser Gly Gln Tyr Leu Leu
 210 215 220
 Thr Leu Lys Ile Gly Arg Phe Ala Gln Thr Ala Leu Val Thr Leu Glu
 225 230 235 240
 Val Asn Asp Arg Cys Leu Lys Ile Gly Ser Gln Leu Asn Phe Leu Pro

00490" 543360

245								250					255			
Ser	Lys	Cys	Trp 260	Thr	Thr	Glu	Gln	Tyr 265	Gln	Thr	Gly	Phe	Gln 270	Gly	Glu	
His	Leu	Tyr 275	Pro	Ile	Ala	Asp	Thr 280	Asn	Thr	Arg	His	Ala 285	Asp	Asp	Val	
Tyr	Arg 290	Gly	Tyr	Glu	Asp	Ile 295	Leu	Gln	Arg	Trp	Asn 300	Asn	Leu	Leu	Arg	
Lys 305	Lys	Asn	Pro	Ser	Ala 310	Pro	Asp	Pro	Arg	Pro 315	Asp	Ser	Val	Pro	Gln 320	
Glu	Ile	Pro	Ala	Val 325	Thr	Lys	Lys	Ala	Glu 330	Gly	Arg	Thr	Pro	Asp 335	Ala	
Glu	Ser	Ser	Glu 340	Lys	Lys	Ala	Pro	Pro 345	Glu	Asp	Ser	Glu	Asp 350	Asp	Met	
Gln	Ala	Glu 355	Ala	Ser	Gly	Glu	Asn 360	Pro	Ala	Ala	Leu	Pro 365	Glu	Asp	Asp	
Glu	Val 370	Pro	Glu	Asp	Thr	Glu 375	His	Asp	Asp	Pro	Asn 380	Ser	Asp	Pro	Asp	
Tyr 385	Tyr	Asn	Asp	Met	Pro 390	Ala	Val	Ile	Pro	Val 395	Glu	Glu	Thr	Thr	Lys 400	
Ser	Ser	Asn	Ala	Val 405	Ser	Met	Pro	Ile	Phe 410	Ala	Ala	Phe	Val	Ala 415	Cys	
Ala	Val	Ala	Leu 420	Val	Gly	Leu	Leu	Val 425	Trp	Ser	Ile	Val	Lys 430	Cys	Ala	
Arg Ser																
<210> 5																
<211> 362																
<212> PRT																
<213> Infectious Laryngotracheitis Virus																
<400> 5																
Met 1	Ala	Ser	Leu	Leu 5	Gly	Thr	Leu	Ala	Leu 10	Leu	Ala	Ala	Thr	Leu 15	Ala	
Pro	Phe	Gly	Ala 20	Met	Gly	Ile	Val	Ile 25	Thr	Gly	Asn	His	Val 30	Ser	Ala	
Arg	Ile	Asp 35	Asp	Asp	His	Ile	Val 40	Ile	Val	Ala	Pro	Arg 45	Pro	Glu	Ala	
Thr	Ile 50	Gln	Leu	Gln	Leu	Phe 55	Phe	Met	Pro	Gly	Gln 60	Arg	Pro	His	Lys	
Pro 65	Tyr	Ser	Gly	Thr	Val 70	Arg	Val	Ala	Phe	Arg 75	Ser	Asp	Ile	Thr	Asn 80	
Gln	Cys	Tyr	Gln	Glu 85	Leu	Ser	Glu	Glu	Arg 90	Phe	Glu	Asn	Cys	Thr 95	His	
Arg	Ser	Ser	Ser 100	Val	Phe	Val	Gly	Cys 105	Lys	Val	Thr	Glu	Tyr 110	Thr	Phe	
Ser	Ala	Ser 115	Asn	Arg	Leu	Thr	Gly 120	Pro	Pro	His	Pro	Phe 125	Lys	Leu	Thr	
Ile	Arg	Asn	Pro	Arg	Pro	Asn	Asp	Ser	Gly	Met	Phe	Tyr	Val	Ile	Val	

130					135					140					
Arg 145	Leu	Asp	Asp	Thr	Lys 150	Glu	Pro	Ile	Asp	Val 155	Phe	Ala	Ile	Gln	Leu 160
Ser	Val	Tyr	Gln	Phe 165	Ala	Asn	Thr	Ala	Ala 170	Thr	Arg	Gly	Leu	Tyr 175	Ser
Lys	Ala	Ser	Cys 180	Arg	Thr	Phe	Gly	Leu 185	Pro	Thr	Val	Gln	Leu 190	Glu	Ala
Tyr	Leu	Arg 195	Thr	Glu	Glu	Ser	Trp 200	Arg	Asn	Trp	Gln	Ala 205	Tyr	Val	Ala
Thr	Glu 210	Ala	Thr	Thr	Thr	Ser 215	Ala	Glu	Ala	Thr	Thr 220	Pro	Thr	Pro	Val
Thr 225	Ala	Thr	Ser	Ala	Ser 230	Glu	Leu	Glu	Ala	Glu 235	His	Phe	Thr	Phe	Pro 240
Trp	Leu	Glu	Asn	Gly 245	Val	Asp	His	Tyr	Glu 250	Pro	Thr	Pro	Ala	Asn 255	Glu
Asn	Ser	Asn	Val 260	Thr	Val	Arg	Leu	Gly 265	Thr	Met	Ser	Pro	Thr 270	Leu	Ile
Gly	Val 275	Thr	Val	Ala	Ala	Val	Val 280	Ser	Ala	Thr	Ile	Gly 285	Leu	Val	Ile
Val 290	Ile	Ser	Ile	Val	Thr	Arg 295	Asn	Met	Cys	Thr	Pro 300	His	Arg	Lys	Leu
Asp 305	Thr	Val	Ser	Gln	Asp 310	Asp	Glu	Glu	Arg	Ser 315	Gln	Thr	Arg	Arg	Glu 320
Ser	Arg	Lys	Phe	Gly 325	Pro	Met	Val	Ala	Cys 330	Glu	Ile	Asn	Lys	Gly 335	Ala
Asp	Gln	Asp	Ser 340	Glu	Leu	Val	Glu	Leu 345	Val	Ala	Ile	Val	Asn 350	Pro	Ser
Ala	Leu	Ser 355	Ser	Pro	Asp	Ser	Ile	Lys	Met						

09881457 061401
F04790" 4548860